

AMENDMENTS TO THE CLAIMS

1-19. (Canceled)

20. (Currently amended) A ~~conifer~~ Loblolly pine tree breeding method comprising:

(a) mixing pollen obtained from a breeding group comprising a plurality of parental ~~conifer~~ Loblolly pine trees to obtain a pollen polymix;

(b) pollinating female reproductive structures from each parental ~~conifer~~ Loblolly pine tree in the plurality of ~~conifer~~ Loblolly pine parental trees with the pollen polymix to obtain a plurality of progeny lots, wherein each progeny lot comprises seeds obtained from a different cross between the pollen polymix and each different ~~conifer~~ Loblolly pine parental tree of the plurality of ~~conifer~~ Loblolly pine parental trees;

(c) evaluating progeny ~~conifer~~ Loblolly pine trees grown from each of the progeny lots using objective criteria to obtain a phenotype score;

(d) determining the pedigree of a plurality of ~~conifer~~ Loblolly pine progeny trees using DNA analysis;

(e) using the pedigree and phenotype score to identify a plurality of elite ~~conifer~~ Loblolly pine trees having an acceptable level of relatedness for inclusion in a breeding group and

(f) using the breeding group identified in step (e) in a next generation of tree breeding to produce an advanced generation of ~~conifer~~ Loblolly pine trees having increased genetic gain.

21. (Currently amended) The method of Claim 20 additionally comprising selecting candidate ~~conifer~~ Loblolly pine trees from within the progeny trees based upon their phenotype score, wherein step (d) is performed on the candidate ~~conifer~~ Loblolly pine trees, and step (e) is

performed using the pedigree and phenotype scores from the candidate ~~conifer~~ Loblolly pine trees to identify elite ~~conifer~~ Loblolly pine trees for use in a the next generation of ~~conifer~~ Loblolly pine tree breeding.

22. (Currently amended) The method of Claim 20, wherein the pedigree and phenotype scores are used to estimate the breeding values of a plurality of progeny and parental ~~conifer~~ Loblolly pine trees, and the breeding values are used to identify the elite ~~conifer~~ Loblolly pine trees for use in the next generation of ~~conifer~~ Loblolly pine tree breeding.

23. (Currently amended) The method of Claim 22, wherein the elite ~~conifer~~ Loblolly pine trees are derived from parental ~~conifer~~ Loblolly pine trees that have a high general combining ability.

24. (Previously presented) The method of Claim 20, wherein the pedigree determined is paternity.

25. (Previously presented) The method of Claim 20, wherein the pedigree determined is paternity and maternity.

26. (Previously presented) The method of Claim 20, wherein the phenotype score is obtained for a phenotype selected from the group consisting of disease resistance, growth rate, growth habit, chemical composition of any plant tissue, drought resistance, temperature hardiness, elevation adaptation, fecundity, and any combination thereof.

27. (Previously presented) The method of Claim 20, wherein the DNA analysis is performed using a DNA analysis method selected from the group consisting of DNA sequencing, restriction fragment length polymorphism (RFLP), amplified fragment length polymorphism

(AFLP), randomly amplified polymorphic DNA (RAPD), single nucleotide repeat microsatellites, di-, tri-, and tetra-nucleotide repeat SSRs, SSR-anchored PCR, sequenced tagged sites (STS), single nucleotide polymorphism (SNP), single stranded conformational polymorphism (SSCP), sequenced characterized amplified regions (SCAR), allele-specific associated primers (ASAP), single primer amplification reaction (SPARs), and cleaved amplified polymorphic sequences (CAP).

28. (Previously presented) The method of Claim 20, wherein a plurality of pollen polymixes are prepared, each pollen polymix comprised of pollen obtained from a plurality of different parental trees, each pollen polymix of the plurality of pollen polymixes being used to pollinate female reproductive structures from parental trees whose pollen or that of its close relatives are not represented in the pollinating pollen polymix.

29. (Previously presented) The method of Claim 20 wherein the DNA analysis method is performed using single nucleotide repeat microsatellite analysis.

30-32. (Canceled)

33. (Currently amended) A tree breeding method comprising:

(a) mixing pollen obtained from a breeding group comprising a plurality of parental ~~loblolly~~ Loblolly pine trees to obtain a pollen polymix;

(b) pollinating female reproductive structures from each parental tree in the plurality of ~~loblolly~~ Loblolly pine parental trees with the pollen polymix to obtain a plurality of progeny lots, wherein each progeny lot comprises seeds obtained from a different cross between the pollen polymix and each different parental tree of the plurality of parental trees;

(c) evaluating progeny ~~loblolly~~ Loblolly pine trees grown from each of the progeny lots using objective criteria to obtain a phenotype score;

(d) determining the pedigree of a plurality of ~~loblolly~~ Loblolly pine progeny trees using DNA analysis; and

(e) using the pedigree and phenotype score to identify a plurality of elite ~~loblolly~~ Loblolly pine trees having an acceptable level of relatedness for inclusion in a breeding group for use in a next generation of tree breeding to produce an advanced generation of ~~loblolly~~ Loblolly pine trees having increased genetic gain.

34. (Previously presented) The method of Claim 33, wherein the DNA analysis is performed using a DNA analysis method selected from the group consisting of DNA sequencing, restriction fragment length polymorphism (RFLP), amplified fragment length polymorphism (AFLP), randomly amplified polymorphic DNA (RAPD), single nucleotide repeat microsatellites, di-, tri-, and tetra-nucleotide repeat SSRs, SSR-anchored PCR, sequenced tagged sites (STS), single nucleotide polymorphism (SNP), single stranded conformational polymorphism (SSCP), sequenced characterized amplified regions (SCAR), allele-specific associated primers (ASAP), single primer amplification reaction (SPARs), and cleaved amplified polymorphic sequences (CAP).

35. (Previously presented) The method of Claim 33, wherein the DNA analysis method is performed using single nucleotide repeat microsatellite analysis.